

FIG. 1A

GGCTGCCGG

-120

AGGGGGCGCGTGGATGCGGCGGAGCTGGAAGCCTCGAGCAGCCGGCGCCTTCT

CTGGCCCCGGCGCCATATGGCTTGAAGAGCCGTGCCACCCAGTGCCCCACTGCCCCA

-1

1 Met Asp Pro Leu Asn Leu Ser Trp Tyr Asp Asp Asp Leu Glu Arg
ATG GAT CCA CCA CTG AAC AAC CTG TCC TCG TGG TAC GAT GAC GAT CTG GAG AGG
1

* 20 * 30
Gln Asn Trp Ser Arg Pro Phe Asn Gly Ser Glu Gly Lys Ala Asp
CAG AAC TGG AGC CCG CCG CCC TTC AAT GGG TCA GAA GAG GCA GAC
90

40
Arg Pro His Tyr Asn Tyr Tyr Ala Met Leu Leu Thr Leu Leu Ile
AGG CCC CAC TAC AAC AAC TAC TAT GCC ATG CTG CTC ACC CTC CTC ATC

50 60
Phe Ile Ile Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser
TTT ATC ATC GTC TTT GGC AAT-GTG CTG GTG TGC ATG GCT GTA TCC
180

Arg	Glu	Lys	Ala	Leu	Gln	Thr	Thr	Thr	Asn	Tyr	Leu	Ile	Val	Ser	
GCA	GAG	AAG	GCT	TTG	CAG	ACC	ACC	ACC	AAC	TAC	TTG	ATA	GTC	AGC	
									70						
Leu	Ala	Val	Ala	Asp	Leu	Leu	Val	Ala	Thr	Leu	Val	Met	Pro	Trp	
CTT	GCT	GTG	GCT	GAT	CTT	CTG	GTG	GCC	ACA	CTG	GTA	ATG	CCG	TGG	
															90
Val	Val	Tyr	Leu	Glu	Val	Val	Gly	Glu	Trp	Lys	Phe	Ser	Arg	Ile	
GTT	GTC	TAC	CTG	GAG	GTG	GTG	GGT	GAG	TGG	AAA	TTC	AGC	AGG	ATT	
									100						
His	Cys	Asp	Ile	Phe	Val	Thr	Leu	Asp	Val	Met	Met	Cys	Thr	Ala	
CAC	TGT	GAC	ATC	TTT	GTC	ACT	CTG	GAT	GTC	ATG	ATG	TGC	ACA	GCA	
															120
Ser	Ile	Leu	Asn	Leu	Cys	Ala	Ile	Ser	Ile	Asp	Arg	Tyr	Thr	Ala	
AGC	ATC	CTG	AAC	CTG	TGT	GCC	ATC	AGC	ATT	GAC	AGG	TAC	ACA	GCT	
									130						360
Val	Ala	Met	Pro	Met	Leu	Tyr	Asn	Thr	Arg	Tyr	Ser	Ser	Lys	Arg	
GTG	GCA	ATG	CCC	ATG	CTG	TAT	AAC	ACA	CGC	TAC	AGC	TCC	AAG	CGC	
															450

FIG. 1B

Arg Val Thr Val Met Ile Ala Ile Val Trp	160	Val Leu Ser Phe Thr
CGA GTT ACT GTC ATG ATT GCC ATT GTC TGG		GTC CTG CTC TCC TTC ACC
Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn	170	Asn Thr Asp Gln
ATC TCC TGC CCA CTG CTC TTC GGA CTC AAC		AAT ACA GAC CAG
Glu Cys Ile Ile Ala Asn Pro Ala Phe Val	180	Tyr Ser Ser Ile
GAG TGT ATC ATT GCC GGC AAC CCT GCC TTT GTG	190	GTC TAC TCC TCC ATT
Val Ser Phe Tyr Val Pro Phe Ile Val Thr	200	Leu Leu Val Tyr
GTC TCA TTC TAC GTG GTG CCC TTC ATC GTC		CTG CTG TAT ATC
Lys Ile Tyr Ile Val Leu Arg Lys Arg Arg	210	Lys Arg Val Asn Thr
AAA ATC TAC ATC GTC GTC CTC CTC CGG AAG CGC	220	AAG CGG GTC AAC ACC
Lys Arg Ser Ser Arg Ala Phe Arg Arg Ala Asn	230	Leu Thr Pro Leu
AAG CGC AGC AGT CGA CGA GCT TTC AGA GCC AAC		CTG AAG ACA CCA CTC

FIG. 1C

Lys Asp Ala Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu
 AAG GAT GCT GCC CGC CGA GCT CAG GAG CTG GAA ATG GAG ATG CTG

Ser Ser Thr Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro
 TCA AGC ACC AGC CCC CCA GAG AGG ACC CGG TAT AGC CCC ATC CCT

Pro Ser His His Gln Leu Thr Leu Pro Asp Pro Ser His His Gly
 CCC AGT CAC CAC CAG CTC ACT CTC CCT GAT CCA TCC CAC CAC GGC

Leu His Ser Asn Pro Asp Ser Pro Ala Lys Pro Gly Lys Asn Gly
 CTA CAT AGC AAC CCT GAC AGT CCT GCC GCC AAA CCA GAG AAG AAT GGG

His Ala Lys Ile Val Asn Pro Arg Ile Ala Lys Phe Phe Glu Ile
 CAC GCC AAG ATT GTC AAT CCC AGG ATT GCC AAG TTC TTT GAG ATC

Gln Thr Met Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr Met
 CAG ACC ATG CCC AAT GGC AAA ACC CGG ACC TCC CTT AAG ACG ATG

FIG. 1D

Ser Arg Arg Lys Leu Ser Gln Gln Lys Lys Ala Thr Gln	340
ACC CGC AGA AAG CTC TCC CAG CAG AAG GAG AAA GCC ACT CAG	
Met Leu Ala Ile Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro	360
ATG CTT GCC ATT GTT CTC CTC GGT GTG TTC TTC ATC ATC TGC TGG CTG CCC	
Phe Phe Ile Thr His Ile Leu Asn Ile His Cys Asp Cys Asn Ile	1080
TTC TTC ATC ACG CAC ATC ATC CTG AAT ATA CAC CAC TGT GAT TGC AAC ATC	
Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Trp Leu Gly Tyr Val Asn	390
CCA CCA GTC CTC TAC TAC AGC GCC TTC ACA TGG TGG CTG GGC TAT GTC AAC	
Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Thr Phe Asn Ile Glu Phe	1170
AGT GCC GTC AAC ACC ATC ATC ATC TAC ACC ACC ACC TTC AAC ATC GAG TTC	
Arg Lys Ala Phe Met Lys Ile Leu His Cys	415
CGC AAG GCC TTC ATG AAG ATC TTG CAC TGC TGAGTCTGCCCCCTTGCCTG	
	1264

FIG. 1E

CACAGAGCTGCTTCCCACTCCCTGCCTATGCAGGCCAGACCTCATCCCTGCAAGCTG
TGGCAGAAAGGCCAGATGAACCTTGGCCTTCTCTCGACCCCTGCAGGCCCTGCAGTGTTA
1383
GCTTGGCTCGATGCCCCCTCTCTGCCCCACACACCCCTCATCCTGCCAGGTAAGGCCAGGG
AGACTGGTATCTTACCAGCTCTGGGGTTGGACCCCATGGCTCAGGGCAGCTCACAGAGTGC
1502
CCCTCTCATATCCAGACCCCTGTCTCCTTGGCACCAAGATGCAGCGGCCTTCCTTGACC
TTCCTCTTGGGCACAGAACTAGCTCAGTGGTCGAGCACACCCCTGATCGCTGGCTTGGCC
1621
TGGCCCTTGCCTTGCCCGGATCAGGTGGTGGGAGGGAGCGACAGTTCTTACTTT
ATAGGAACCACATAGGAAAGCAGGGAACACGCCAAGTCCTCCAGGCACATCAGTGTCAAG
1740
AGACACACATAAACACCCAGGTAGCTCCATGGACCCAGAGAACTGAGGCTGAAAAATC
TGTTTCCACTCCAACCTAGTGTGAGTCCCTACTTTTCATAGCCATGGGTATTACTATG
1859

FIG. 1F

TCCTACCTTGTTATAGTATCCCATGGGGTTTCTGTACCATTTGGGGGAAACAACTCTA
 ATCCTCAAGGGCCCAAGAGAAATCTGTAAAGGAGAAAAATAGGCTGATCTCCCTCTACTCT
 1978
 CCAATCCACTCCACCACCTTCTTGATATACCTTGGATGTATCCATTCCCTCACAGCAAATG
 CTGGCCAGTCAGGCCCTTGGACCAGTGTGGAGTTGAAGCTGGATGTGGTAACTTGGGGCT
 2097
 CTTTGGGGCTGGGGGGTGTAAACATCGTCTCTCTTCCATATCTCTTCCCTTCCCAGTG
 CCTCTGCCCTAGAAAGAGGCTGTGGATGGGGTGCTGGGACTGCTGATACCATTTGGGCCCTGG
 2216
 CCCTGAATCAGGAGGGGAAGCTGCAGTTTGGAGGGTTCTGGGATCCAACTCTGTAAACAT
 CACTATACCTGTACCAAAACTAAAAACCTTGACAAGAGTCAAAAAA
 2317

FIG. 1G

MD... [PL]... [NIS]WYDDDLERQNWSPFNGSEKADRPYNYAMIT[LL]... IFII[FVGNVLVCM]AVSREKALQ[TT]TNY
 MGP... [P]... GNDSDFLLTNGSHV... PDHDVTEERDEAWVVGMAIT[MSVIVLAI]VFGNVLVITAI[AKFERLQ]TTTNY
 MGSQ [PQA]GNASWNGTEAPG... GGARATPYSLQVT... LTLVCLAGLL... MLLTVFGNVLVITAI[AVFTSRAT]KAPQNL
 MDVLS [PGQ]QNNTTSPAPFE... TCGNTTGISDVTVSQV.ITSLIT[GL]... IFCAVITGNAGVVAIALERSLQNVANY
 MNTSAPPAVSPNITVLAP... GKGPWQVA..... FIGITITGLL.SLATITGNLITVITISFKVNTET[KT]VNY
 MGCACV.VMTDINIS..... SGLDSNATGITAFSPMGWQLALWTAAYLAL.VLVAVMGNATVIWII LAHQMRITVNY

D6
B6
X8
G-21
M1
SK

11

LIVSLAMADIIIVATLVMPVVVYLEVGVGVGFSGRIHCDIFVTLDVMMCTASILNLCAISIQRYTAIVAMPIMIVMTRYSSKRR
 FIDLSACADLVMGIAVPPFGASHIIMQVWNGFWCEFTSIQVLCVTASIEITLCUAVQRYIAITSPFKVQSLLTKNKA
 FIVLSASADIIIVATLVIPFSLANEMQVMEGKTWCEIYLALDVLFCISSIVHLCAISIQRYMSITQAIENLKRTPRI
 LIGSLAVTIDIMVSVLVIIPMAALYQVLNNWTLGVQVTCDFIALDVLCTSSILHLCAIAIQRYMAITDPIIDVVKRTPRPR
 FLLSLACADIIIGDFSMNLYTTLMLQVWALGTLACDLWLALDVASNAVMNLIJISFQRYFSVTRPLSYRAKTRPRRA
 FIVNLALADICMAAFNAAFNVYASHNIMVEGRAFCYFQNLFPITAMFVSIYSMTAJAAQRYMAIVRPFQPLRSAPGTR

D₆
B₆
X₆
G-21
M₁
SK

A

VTVMIAVWVISPTISC. PLLFGLNNTD. QNECIANPAFVVYSSIMSFYVPFIVTLVLVYIKIMVLVRKRRKRVNTR- (111)
 RMJ. ILMWVIVSGLTSFPIQMHYRATH. QKAIDCYHRETCDDFTNQAYALWSSIVSFYVPLVWVFVSRVFQVAKRQLQKI- (32)
 KAI. JIITVWVISAIVISFPLISIEKKGG. GGQPAEPRCEINDQKWVWSSICIGSFAPOLIMLVWVRIYQIAKRTRVP- (137)
 ALT. SLT. MLIGLISIPMLGWRTPEDR. SDPDACTISKDMGYTUYSTFGAFYPLILMLVLVGRIFRAARFRIPIT- (110)
 ALM. IGLAWLVSEVLWA. PAILFWQYLVGE. RTVLACQCYIQFLSQPIITFGTAMAAFLYLPVIMCTIMWRIYRETNRAREL- (137)
 AV. IAGIMLVALALAF. PQCFYSTITDEGATKCVVAWPEDSGGKMLLLYHLIVIALIYE. LPQVWVFVMSVIGLTLWRSPVG- (12)

D6
B6
X6
G-21
M1
SK

VI

-KEKKAQTQMTAI VTCMF IICWLPFFITHI IINIHOCN... IPPVLYSAFTWLGYNVSA.. VNPIIYTTFNTEFRNAFMKI IHC
 -KEFKALKTKTIGIMGIFTILCWLPFFIVNIVHVIQDNL... IPKEVYILLNWLGYVNSA.. PNPIIYCRSP.DFRIAFQEI I.LC--(36)
 -REKRFTEFVIAVTCMFVVCWCPFFETYTITAVGCS... VPRITFKFFPWPGYCNSS.. LNPIVITYLFNHFDFRAFMKI I.CRC--(6)
 -REKRTVKTIQTIMGIF IICWLPFFIVALVLPCESSC.. HMPITILGAIINWLGYNSL.. INPVLVAYENKDFQNAFMKI I.KONFCRQ
 -KEKKAARTLSAILLAFIVTMTI VNMVLVSTFCKDC... VPETILWELGYWIGYVNST.. LNPMGYALQNKAFRDTRFL I.IHCR--(24)
 -ARKKFVKTMVIVVVTFAICWLPYHLYFI IIGTFQEDIYCHKFIQVILALPWIA.. MSSI TYNPII IYCCINHRFSQFRLAPROC--(62)

D6
B6
X:
G-21
M1
SK

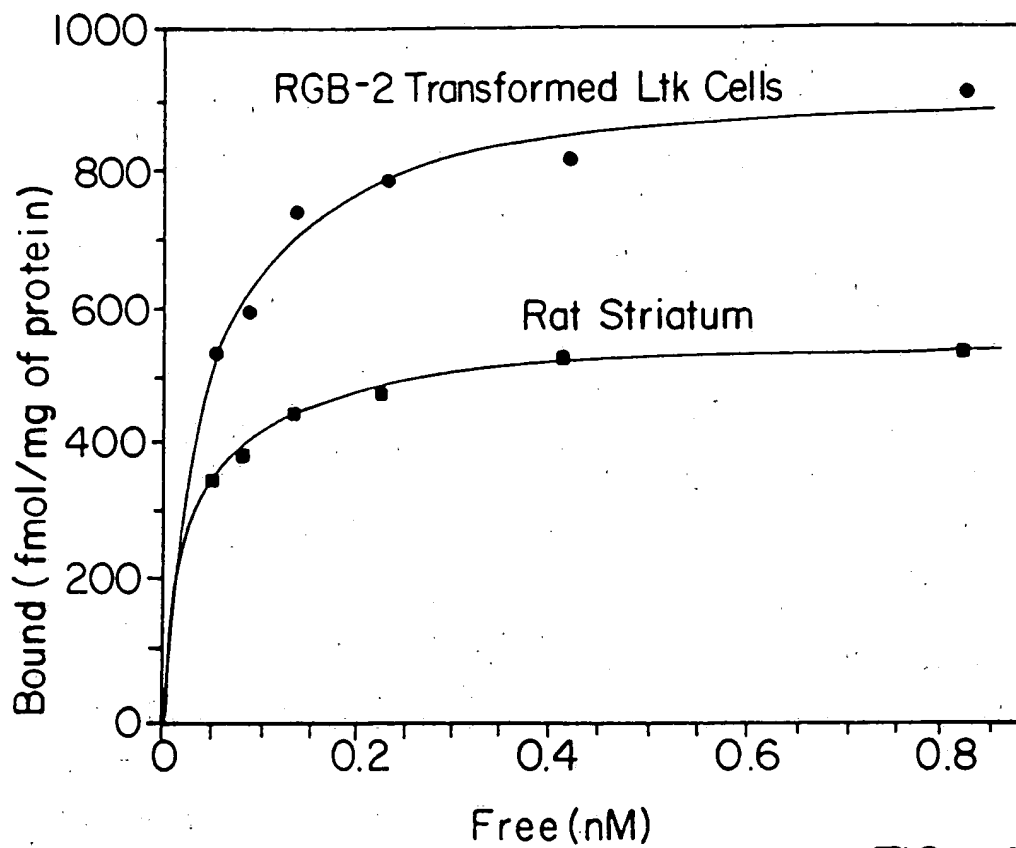


FIG. 4A-1

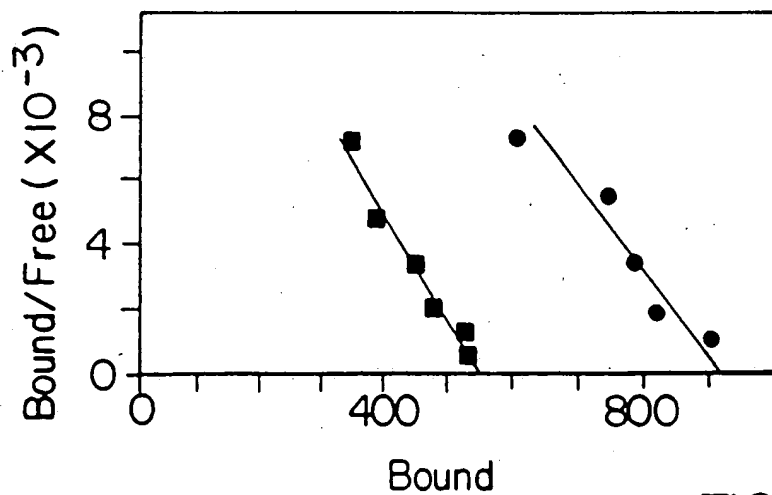
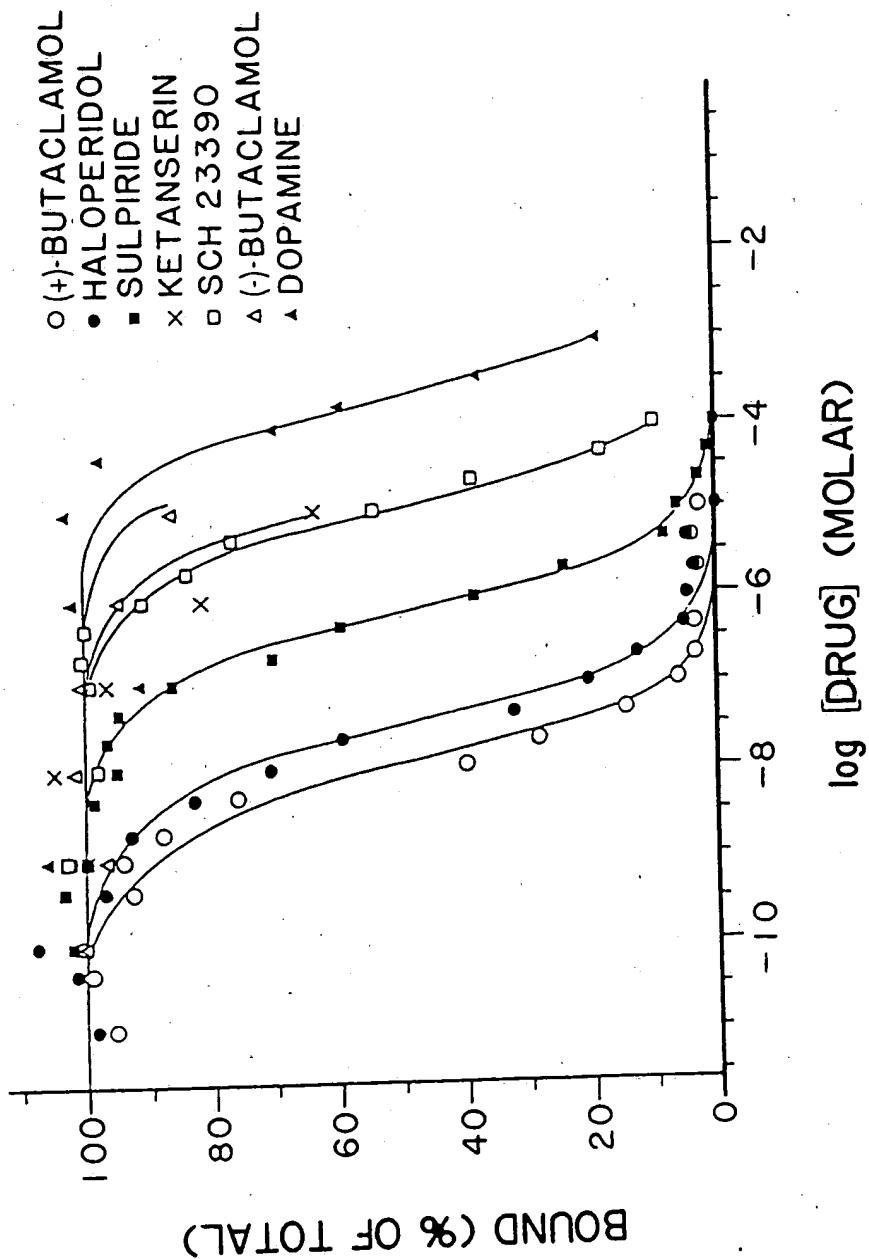


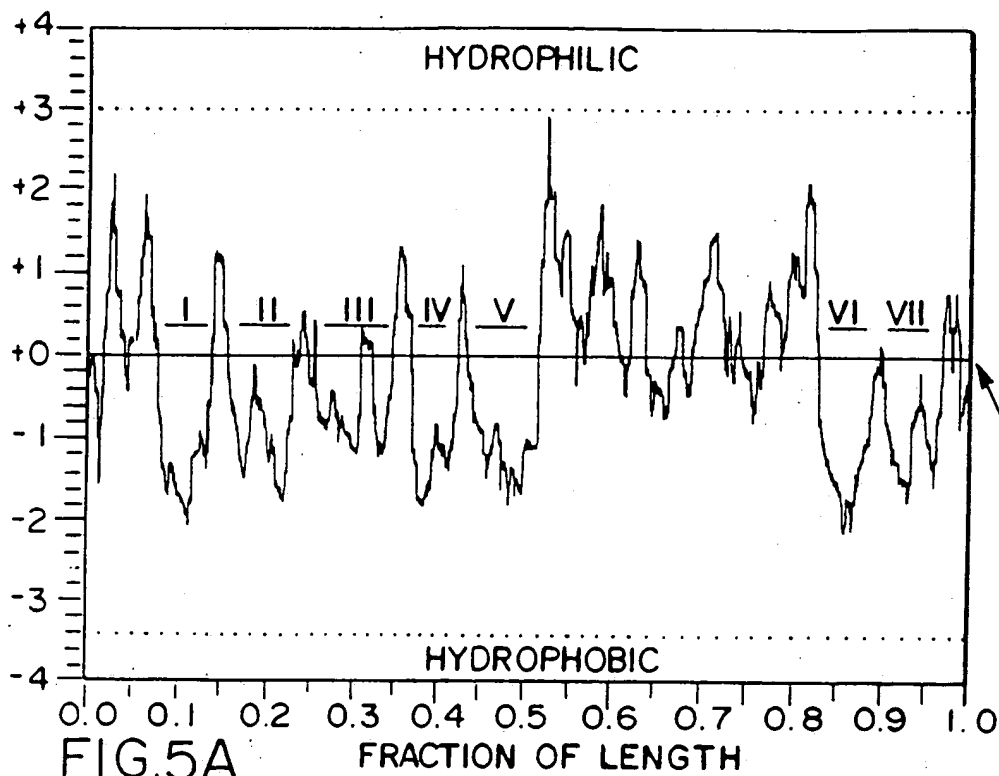
FIG. 4A-2

FIG. 4B



DRUG		Ki (nM)	
		Transformed Ltk-Cells	Rat Striatum
RGB-2			
(+)-Butaclamol	0.83	1.0	
(-)-Butaclamol	>1,000	>1,000	
Haloperidol	3.0	5.3	
Dopamine + GTP	17,000	6,300	
Sulpiride			
high affinity	80	67	(87%)
low affinity	---	>10,000	(13%)
SCH 23390			
high affinity	---	35	(16%)
low affinity	1,000	780	(84%)
Ketanserin			
high affinity	---	27	(25%)
low affinity	>1,000	>1,000	(75%)

FIG. 4C



RGB-2

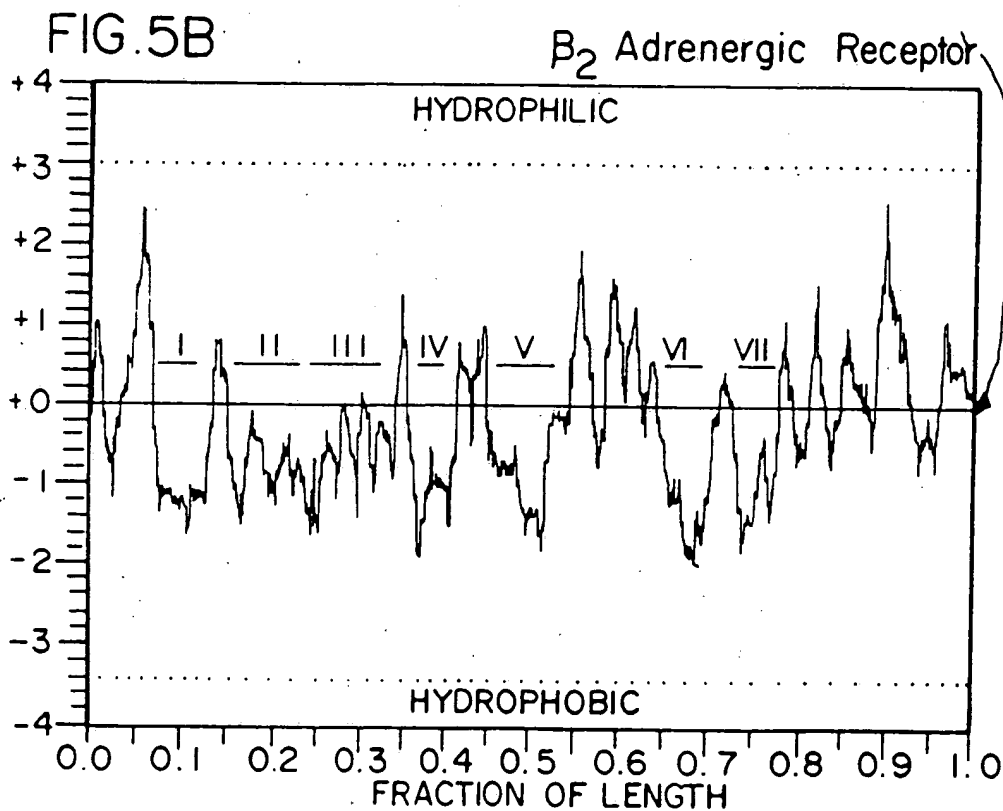
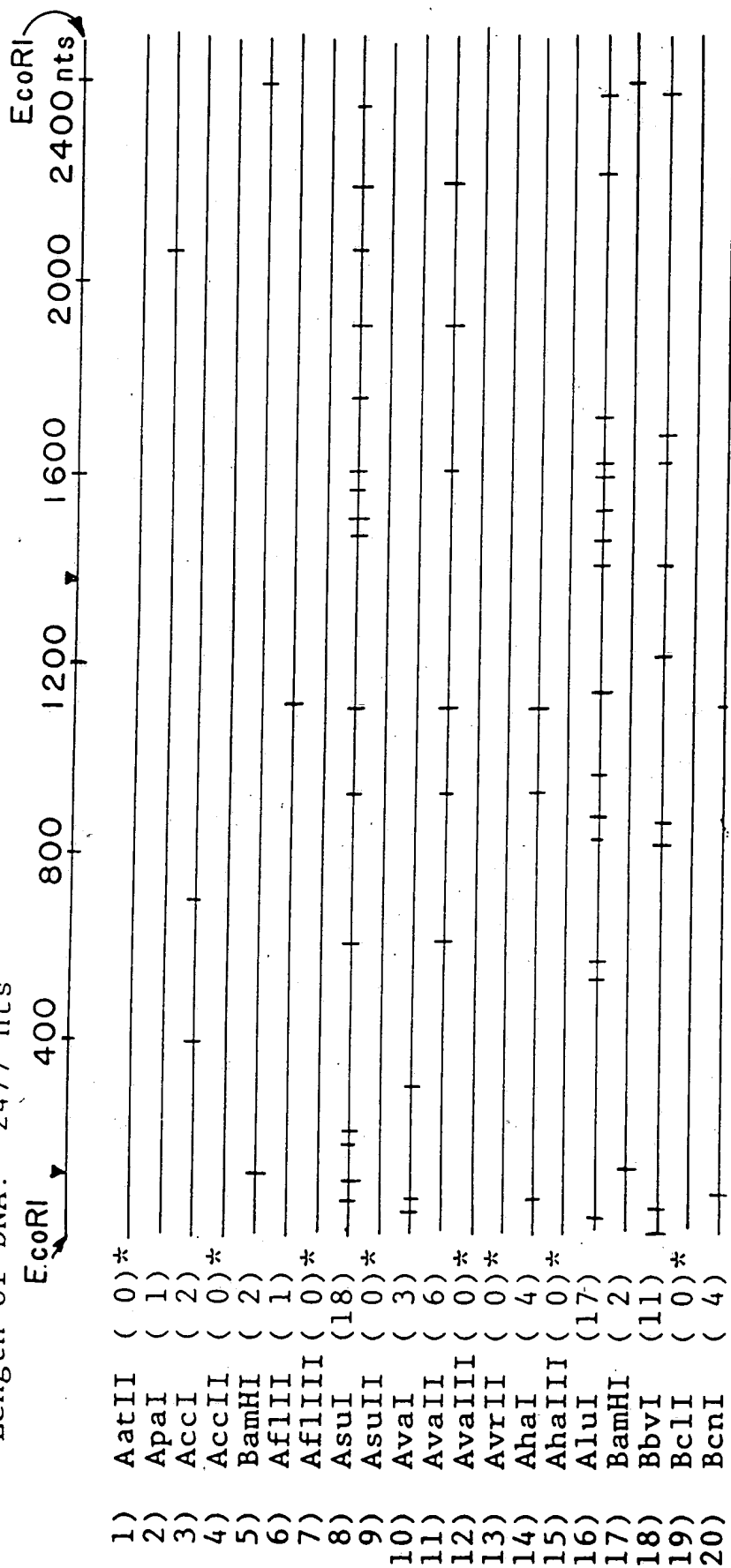


FIG. 6A

Length of DNA: 2477 nts



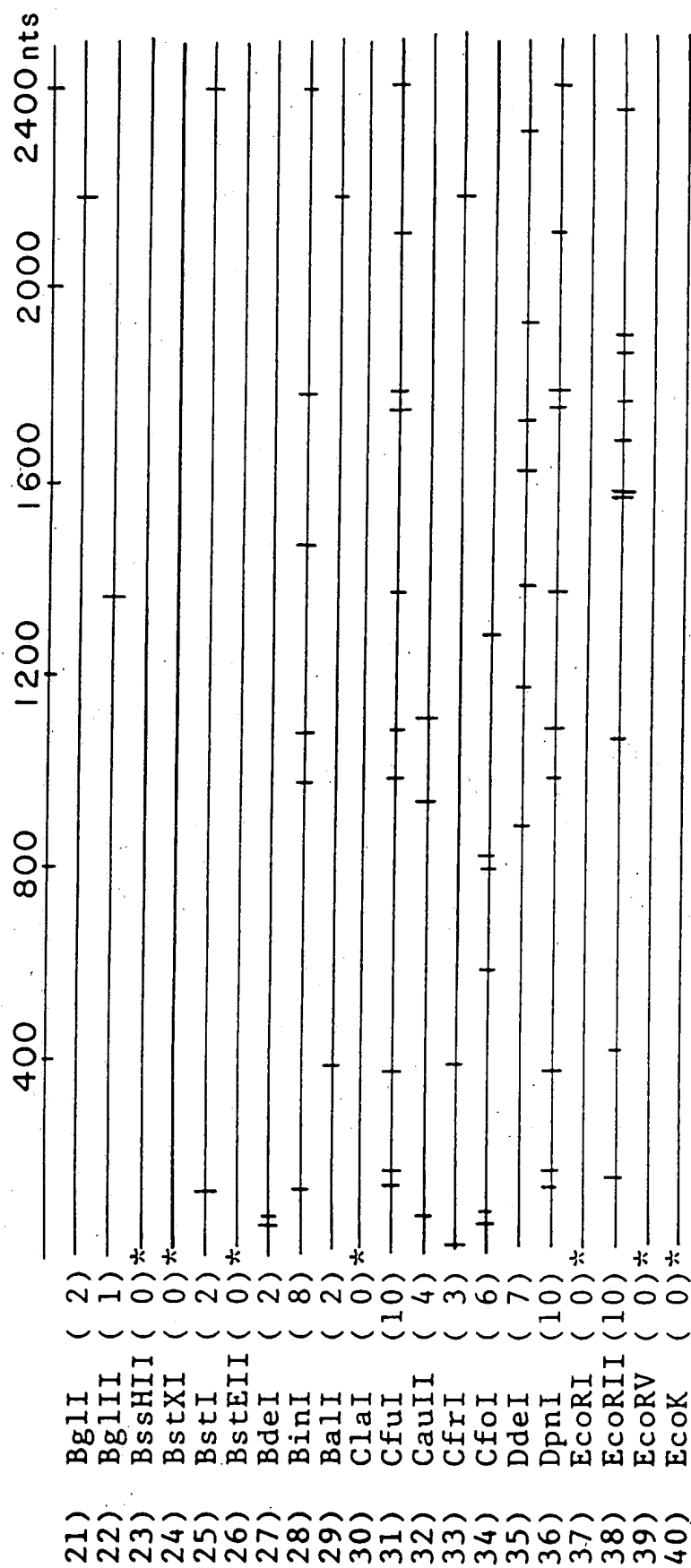


FIG. 6B

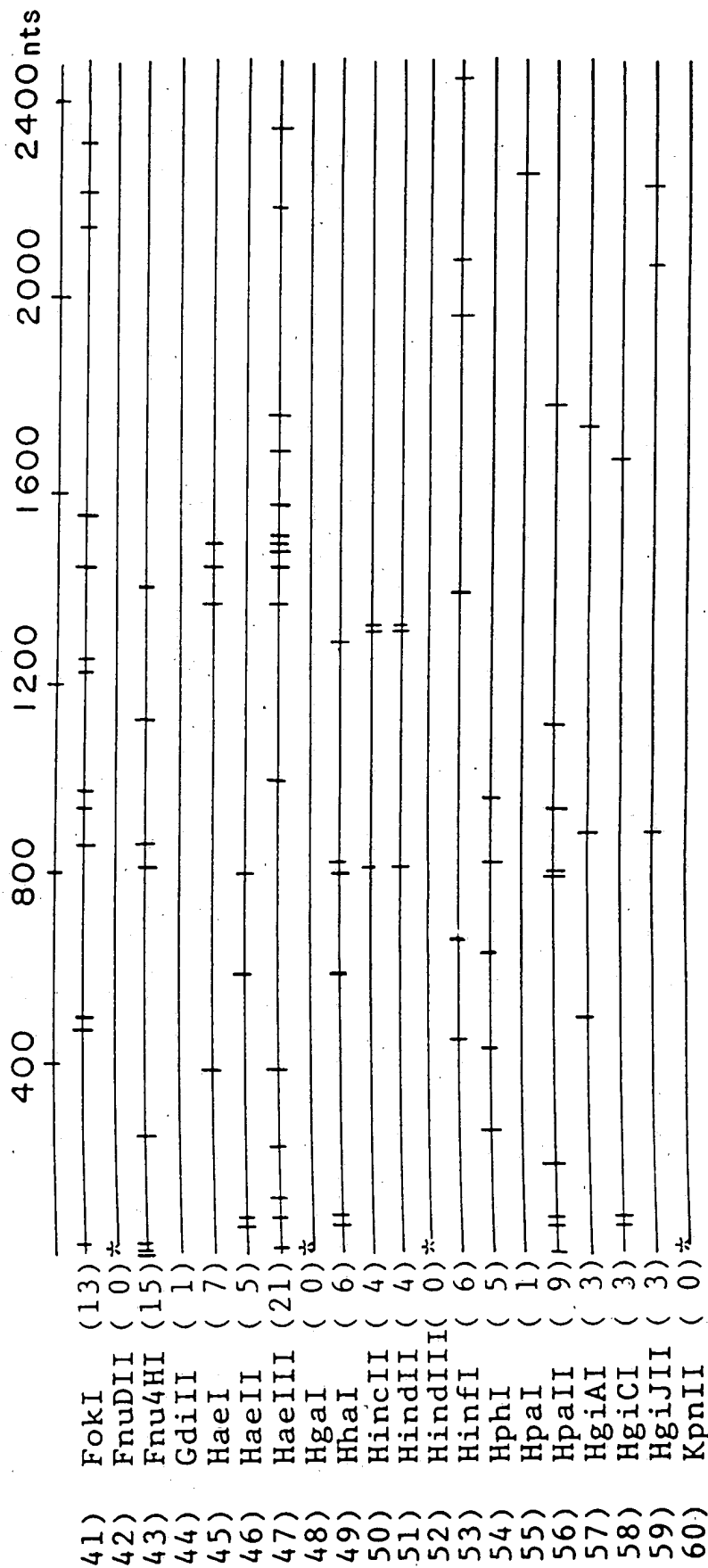


FIG. 6C

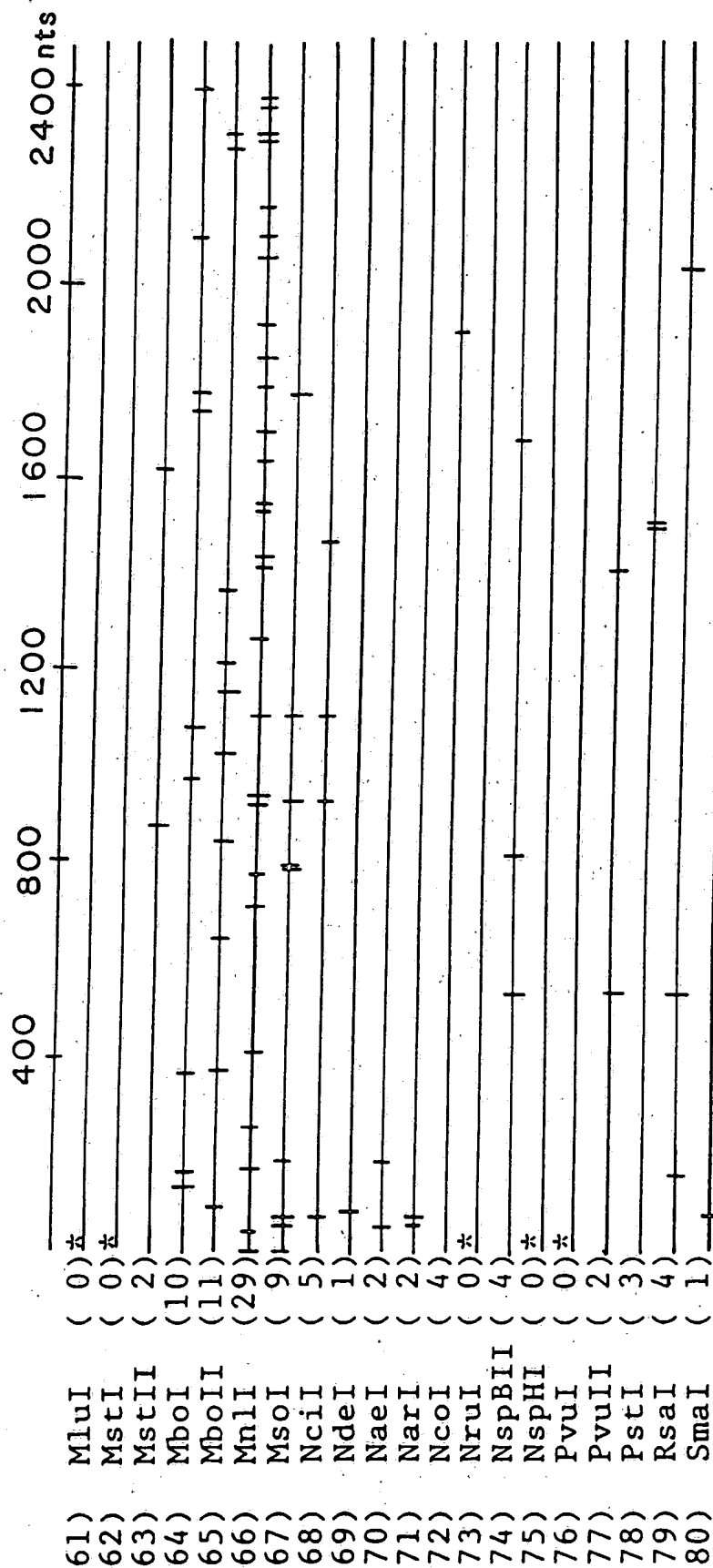


FIG. 6D

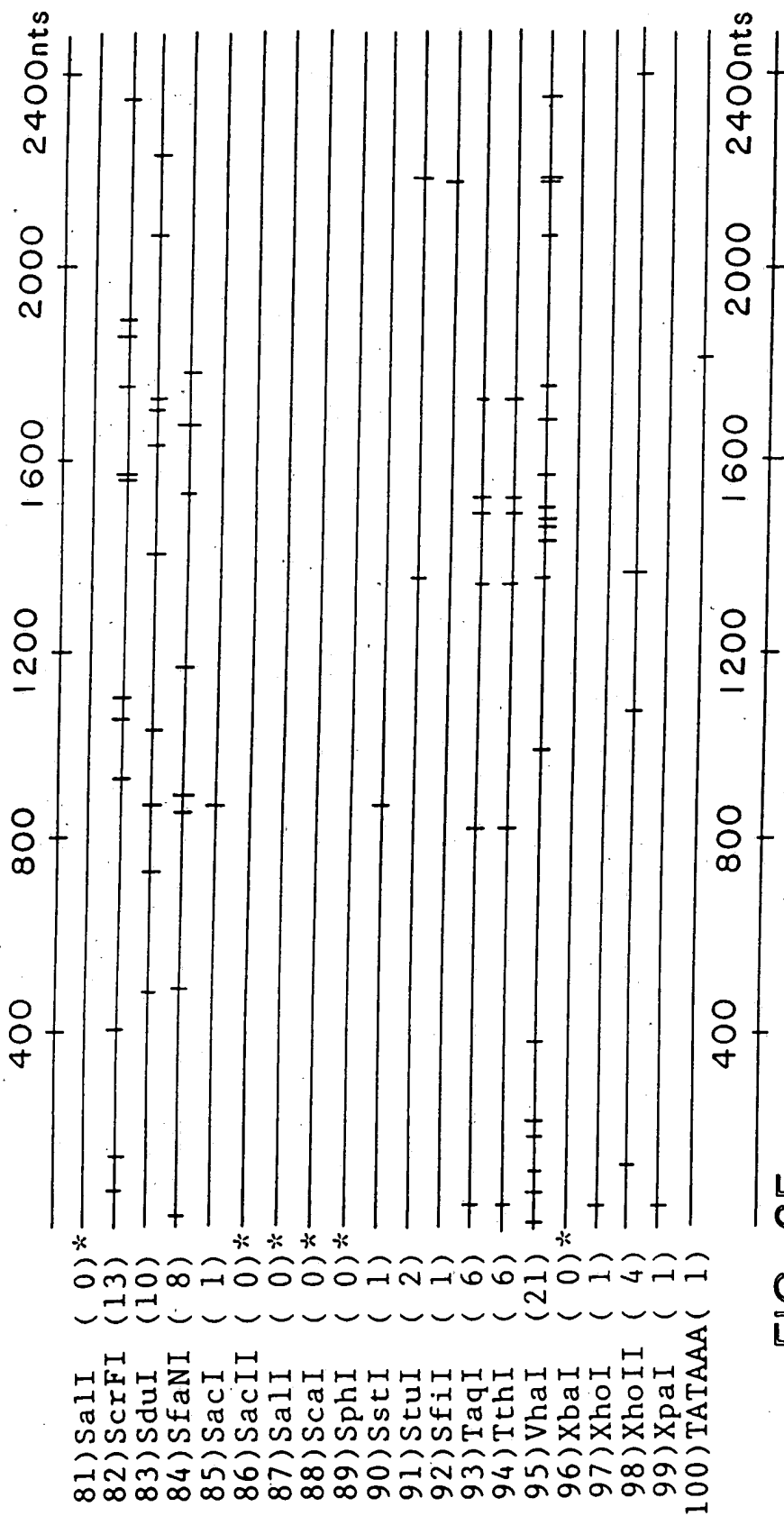


FIG. 6E

FIG. 7A

3' GTC GGG TGG GCT CTC CTG GGC CAT GTC GGG GTA GGG TGG GTC GGT GGT GGT CGA 5' 54
 5' CAG CCC ACC CGA GAG GAC CCG GTA CAG CCC CAT CCC ACC CAG CCA CCA CCA GCT 3'
 Gln Pro Thr Arg Glu Asp Pro Val Gln Pro His Pro Thr Gln Pro Pro Pro Ala
 Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln Leu
 Ala His Pro Arg Gly Pro Gly Thr Ala Pro Ser His Pro Ala Thr Thr Ser

81 108
 CTG AGA GGG GCT GGT CAG GGT GGT ACC AGA GGT GTC GTG AGG GCT GTC GGT GGT GCG
 GAC TCT CCC CGA CCC GTC CCA CCA TGG TCT CCA CAG CAC TCC CGA CAG CCC CGC
 Asp Ser Pro Arg Pro Val Pro Pro Trp Ser Pro Gln His Ser Arg Gln Pro Arg
 Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp Ser Pro Ala
 Leu Ser Pro Thr Arg Pro Thr MET Val Ser Thr Ala Leu Pro Thr Ala Pro Pro

135 162
 GTT TGG TCT CTT CTT ACC CGT ACC GGT ACC GGT TTC CTG GTG GGG TTC CTA ACG GTT CTA
 CAA ACC AGA GAA GAA TGG GCA TGC CAA AAG GAC CAC CCC AAG GAT TGC CAA GAT
 Gln Thr Arg Glu Glu Trp Ala Cys Gln Lys Asp His Pro Lys Asp Cys Gln Asp
 Lys Pro Glu Lys Asn Gly His Ala Lys Arg Thr Thr Pro Arg Ile Ala Lys Ile
 Asn Gln Arg Arg MET Gly MET Pro Lys Gly Pro Pro Gln Gly Leu Pro Arg Ser

189 216
 GAA ACT CTA GGT CTG GTA CCG GTT ACC GTT TTG GGC CTG GAG GGA GTT CTG GTA
 CTT TGA GAT CCA GAC CAT GCC CAA TGG CAA AAC CCG GAC CTC CCT CAA GAC CAT
 Leu . Asp Pro Asp His Ala Gln Trp Gln Asn Pro Asp Leu Pro Gln Asp His
 Phe Glu Ile Gln Thr MET Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr MET

FIG. 7B

CTC GGC ATC CTT C6A G55 GGT CGT CTT CCT CTT TCG GTG AGT CTA CGA GCG	270
GAG CCG TAG GAA G3T C44 CCA GCA GAA GGA GAA AGC CAC TCA GAT GCT CGC	
Glu Pro . Glu C TT Pro Ala Glu Gly Glu Lys Lys Ala Thr Gln MET Leu Ala	
Ser Arg Arg Lys Leu Phe Gln Gln Lys Glu Lys Arg Arg Lys Pro Leu Arg Cys Ser Pro	
Ala Val Gly Ser	
GTA 5CA AGA GCC GCA CAA GTA GTA GAC CGA CGG GAA GAA GTA GTG TGT GTA	324
CAT 4GT TCT CGG CGT GTT CAT CAT CTG CTG GCT GCC CTT CTT CAT CAC ACA CAT	
His T Ser Arg Arg Val His His Leu Leu Ala Ala Leu Leu His His Thr His	
ILE Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile	
le Phe Ser Ala Cys Ser Ser Ser Ala Gly Cys Pro Ser Ser His Thr Ser	
GGA CTT GTA TGT GAC ACT GAC GAC GGT GTA GGG CGG ACA GGA CAT GTC GCG GAA GTG	378
CCT GAA CAT ACA CTG TGA CTG CAA CAT CCC GCG TGT CCT GTA CAG CGC CTT CAC	
Pro Glu His Thr Leu . Leu Gln His Pro Ala Cys Pro Val Gln Arg Leu His	
Leu Asn Ile His Cys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr	
. Thr Tyr Thr Val Thr Ala Thr Ser Arg Leu Ser Cys Thr Ala Pro Ser Arg	
CAC CGA CCC GAT ACA GTT GTC GCG GCA CTT GGG GTA GTA GAT GTG GAA GTT	432
GTG GCT GGG CTA TGT CAA CAG CGC CGT GAA CCC CAT CAT CTA CAC CAC CTT CAA	
Val Ala Gly Leu Cys Gln Gln Arg Arg Glu Pro His His Leu His His Leu Gln	
Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn	
Gly Trp Ala MET Ser Thr Ala Pro . Thr Pro Ser Ser Thr Pro Pro Ser Thr	

459
GTA ACT CAA GGC GTT CCG GAA GGA CTT CTA GGA GGT GAC GAC TGA GAC GAC GGA 486
CAT TGA GTT CCG CAA GGC CTT CCT GAA GAT CCT CCA CTG CTG ACT CTG CTG CCT
His . Val Pro Gln Gly Leu Pro Glu Asp Pro Pro Leu Thr Leu Leu Pro
Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys STOPLeu Cys Cys Leu
Leu Ser Ser Ala Arg Pro Ser . Arg Ser Ser Thr Ala Asp Ser Ala Ala Cys
513
CGG CGT GTC GTC GGA CGA AGG GTG GAG GGA CGG GTC ACG GCC GGT CGG AGT GGG 540
GCC GCA CAG CAG CCT GCT TCC CAC CTC CCT GCC CAG TGC CGG CCA GCC TCA CCC
Ala Ala Gln Gln Pro Ala Ser His Leu Pro Ala Gln Cys Arg Pro Ala Ser Pro
Pro His Ser Ser Leu Leu Pro Thr Ser Leu Pro Ser Ala Gly Gln Pro His Pro
Arg Thr Ala Ala Cys Phe Pro Pro Cys Pro Val Pro Ala Ser Leu Thr Leu
567
AAC GCT TGG CAC TCG TCC TTC CCG ACC CAC CTA GCC GGA GGA GAA GAT CGG GGC 594
TTG CGA ACC GTG AGC AGG AAG GCC TGG GTG GAT CGG CCT CCT CTT CTA GCC CCG
Leu Arg Thr Val Ser Arg Lys Ala Trp Val Asp Arg Pro Pro Leu Leu Ala Pro
Cys Glu Pro . Ala Gly Arg Pro Gly Trp Ile Gly Leu Leu Phe . Pro Arg
Ala Asn Arg Glu Gln Glu Gly Leu Gly Gly Ser Ala Ser Ser Ser Ser Pro Gly

FIG. 7C

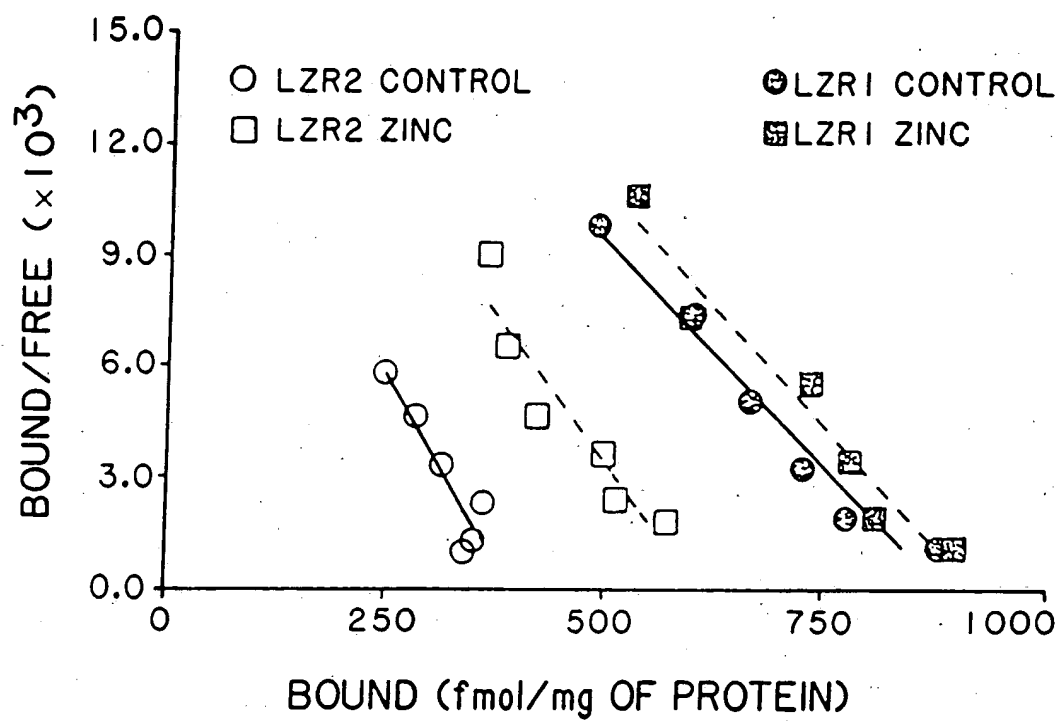


FIG. 8

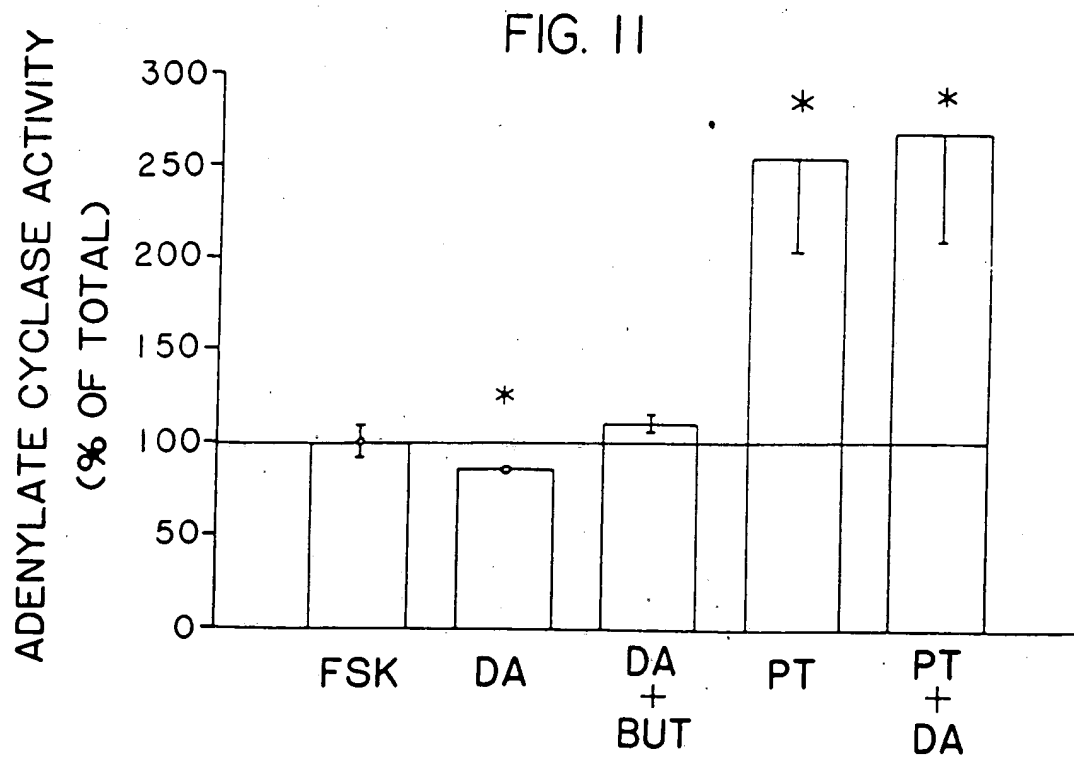


FIG. 9A

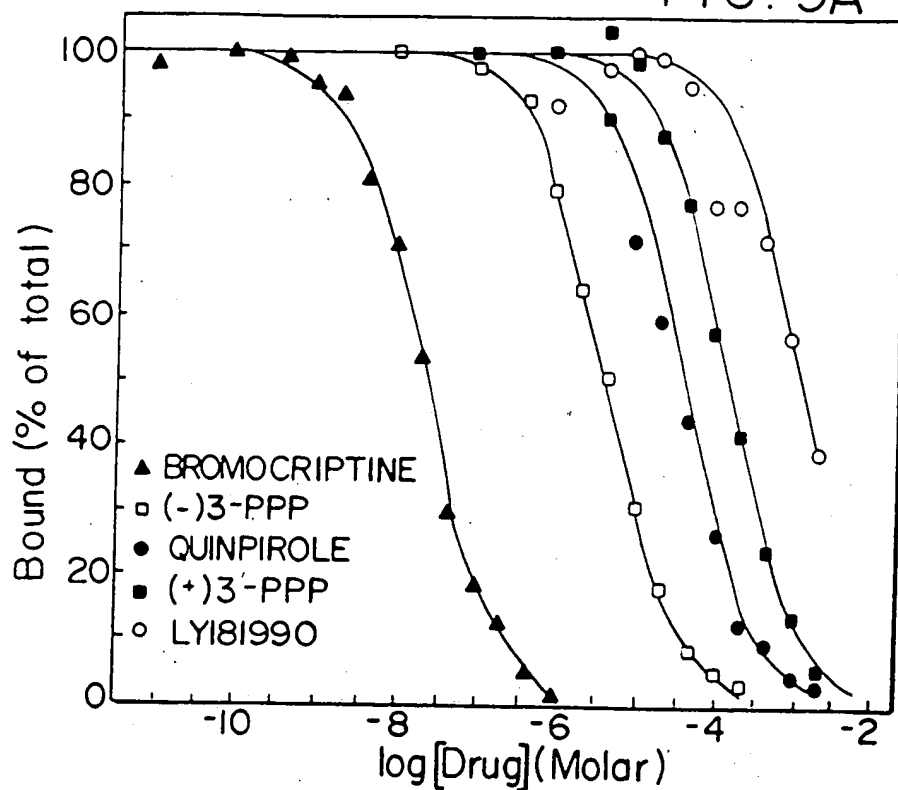
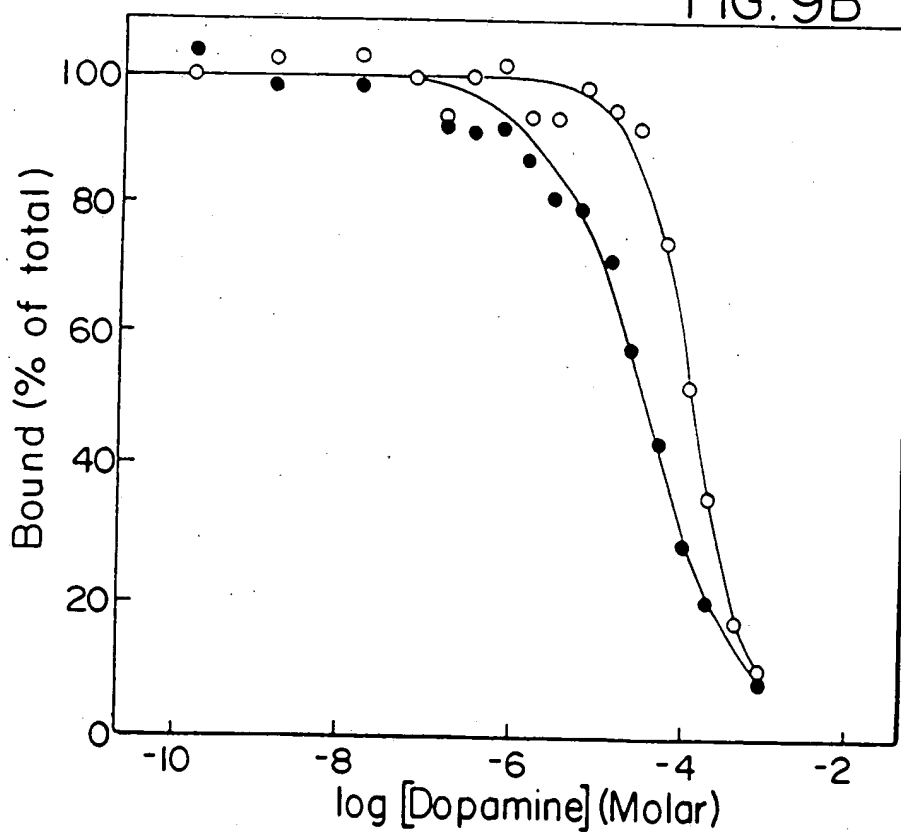


FIG. 9B



12345678910

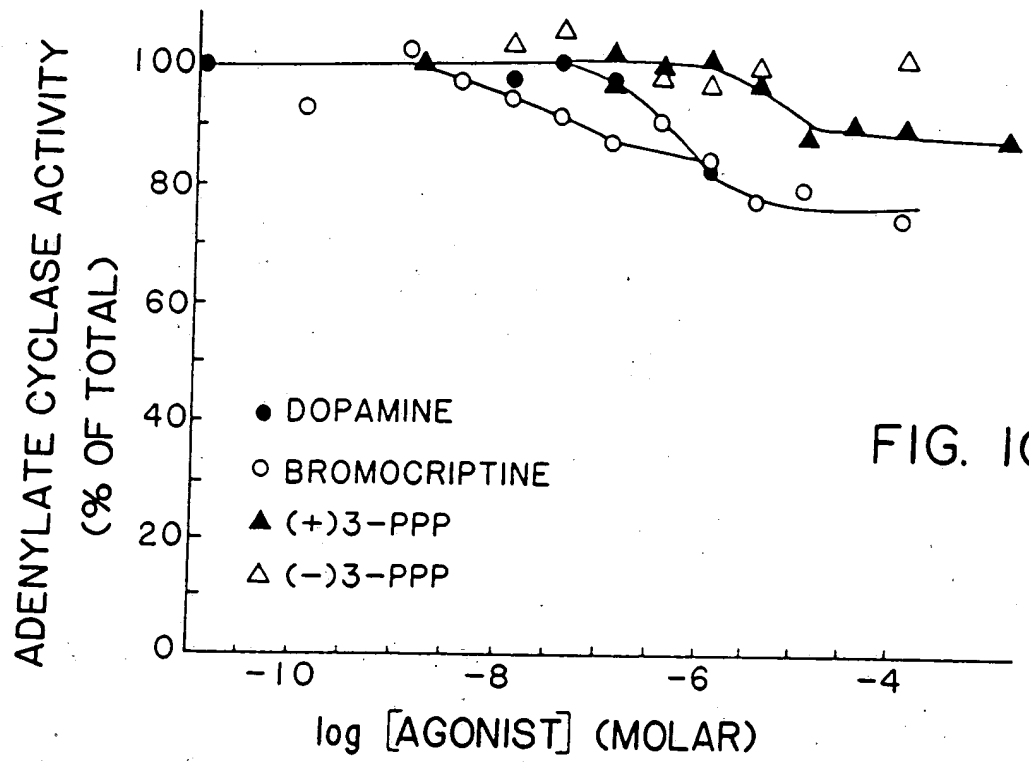


FIG. 10A

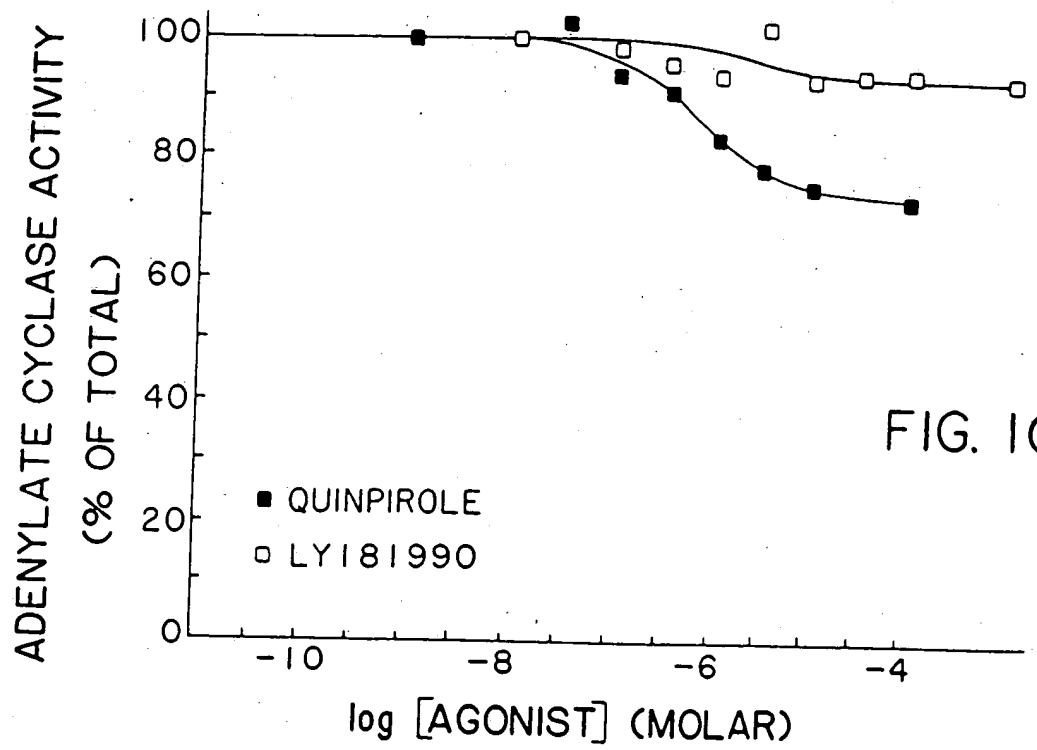


FIG. 10B

CONTROL				+P.T.			
BASAL	FSK	FSK+DA		BASAL	FSK	FSK+DA	
2.1	22.6	14.3		1.7	26.7	23.1	
0.2	2.2	2.1		0.4	2.0	0.5	
—	—	41%		—	—	14%	

FIG. 12A

\bar{X} S.E.

INH

CONTROL				+P.T.			
BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
0.60	2.41	0.32	0.84	0.61	2.68	0.55	2.56
0.02	0.31	0.02	0.13	0.09	0.08	0.03	0.25
—	—	53%	71%	—	—	10%	3%

FIG. 12B

\bar{X} S.E.

INH

CONTROL				+P.T.			
BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
0.78	5.1	0.25	0.76	0.64	5.29	0.66	4.76
0.04	0.4	0.03	0.01	0.01	0.44	0.03	0.16
—	—	68%	88%	—	—	0%	12%

FIG. 12C

\bar{X} S.E.

INH

123456789101112

FIG. 13B-1

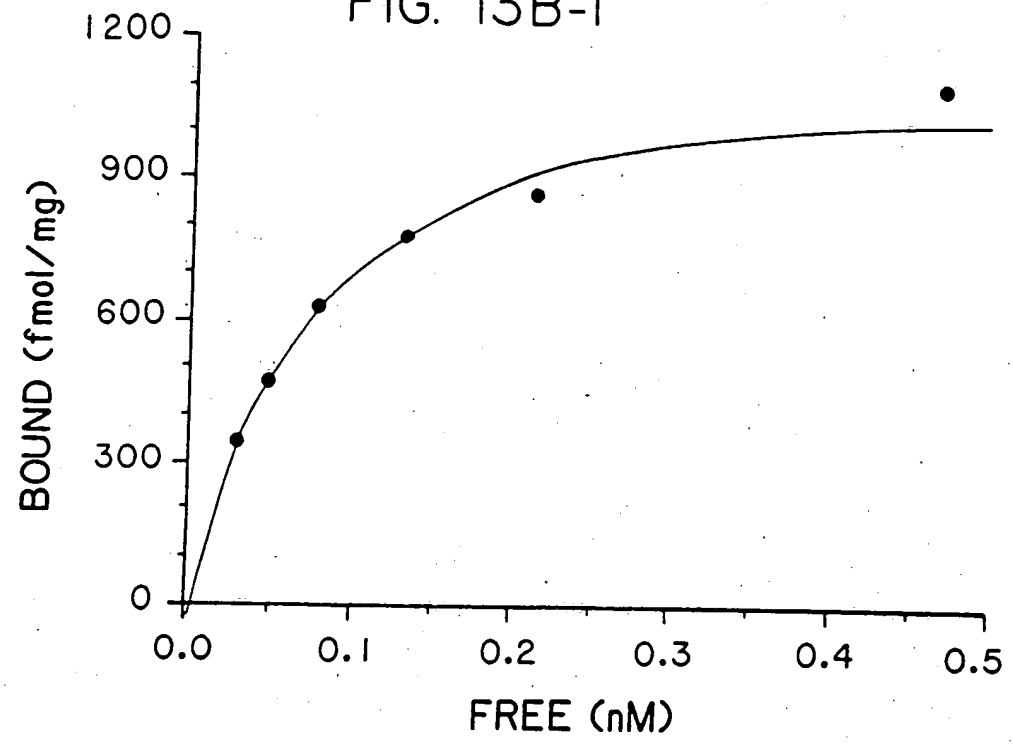


FIG. 13B-2

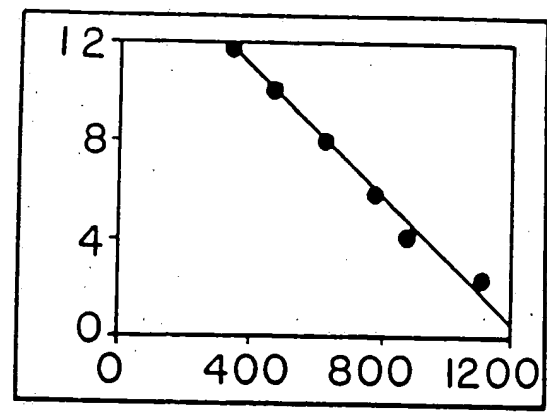
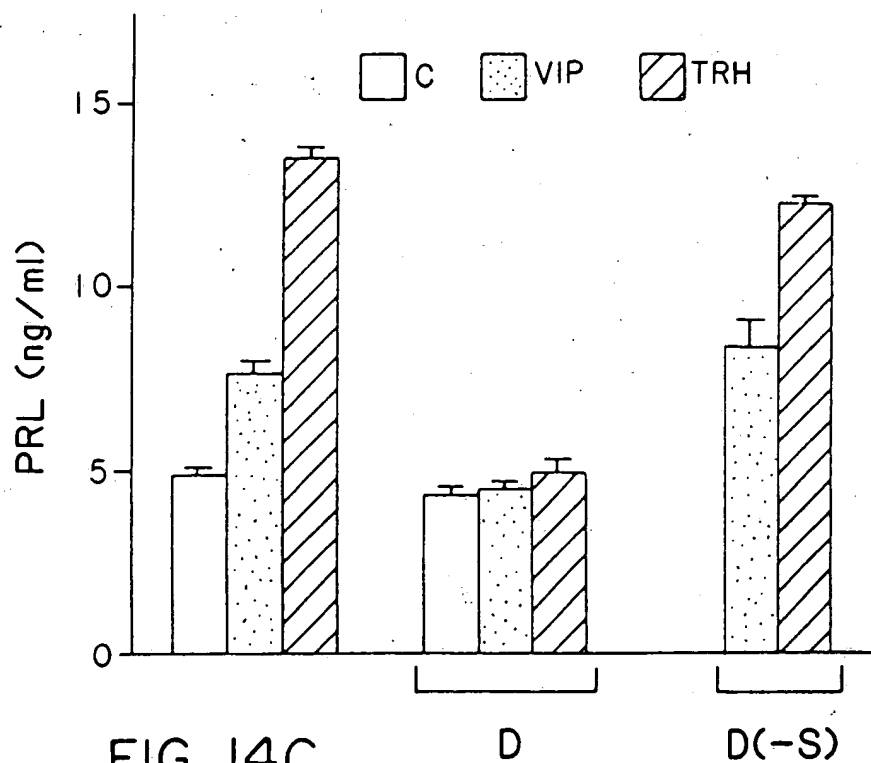
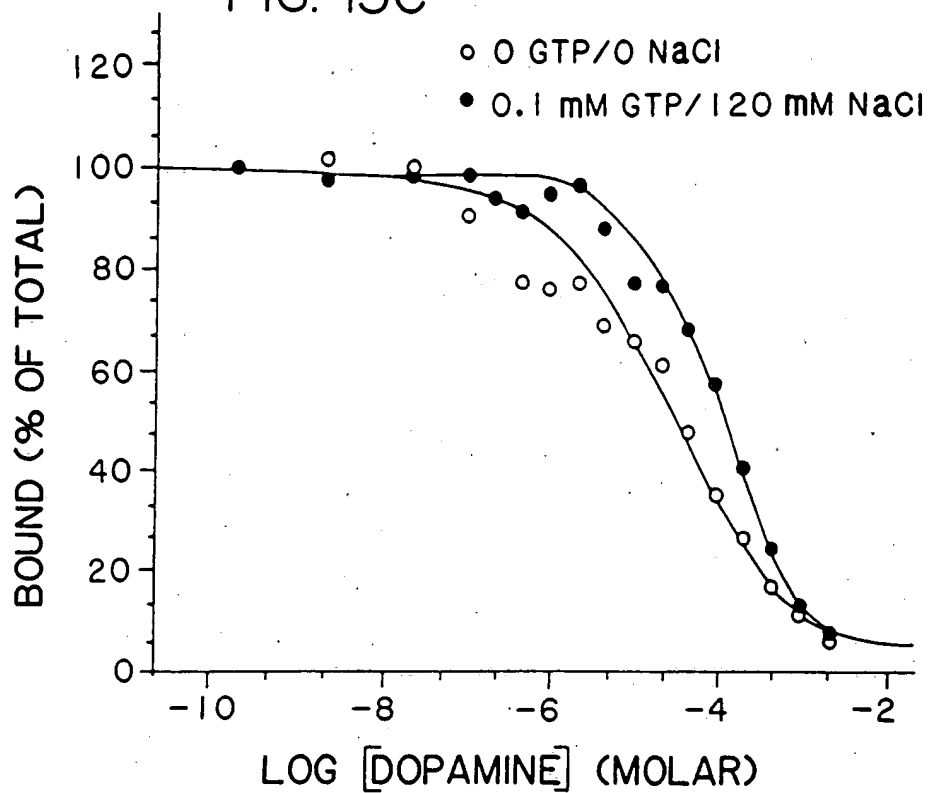


FIG. 13C



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FIG.14A

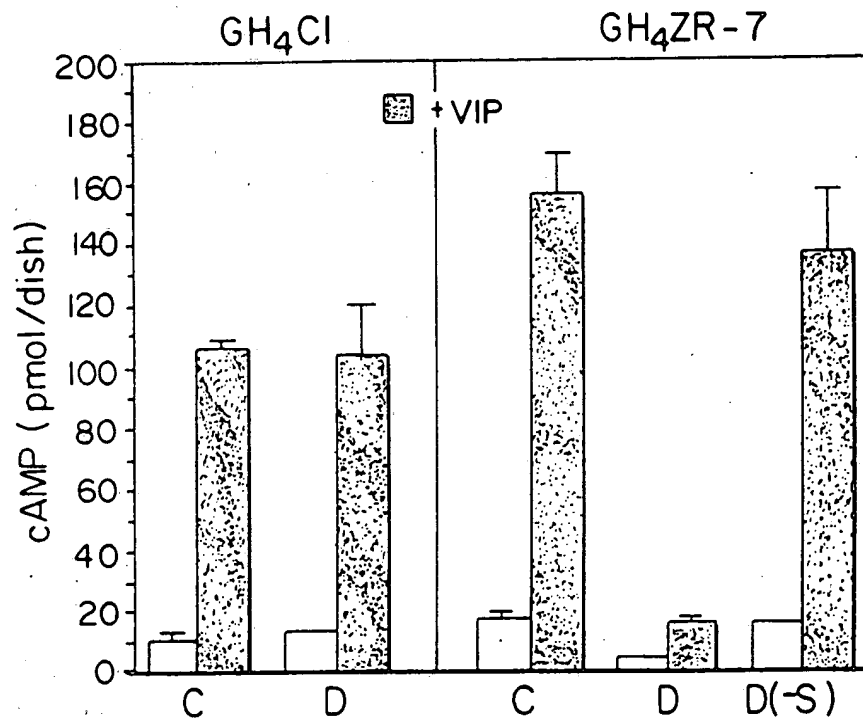
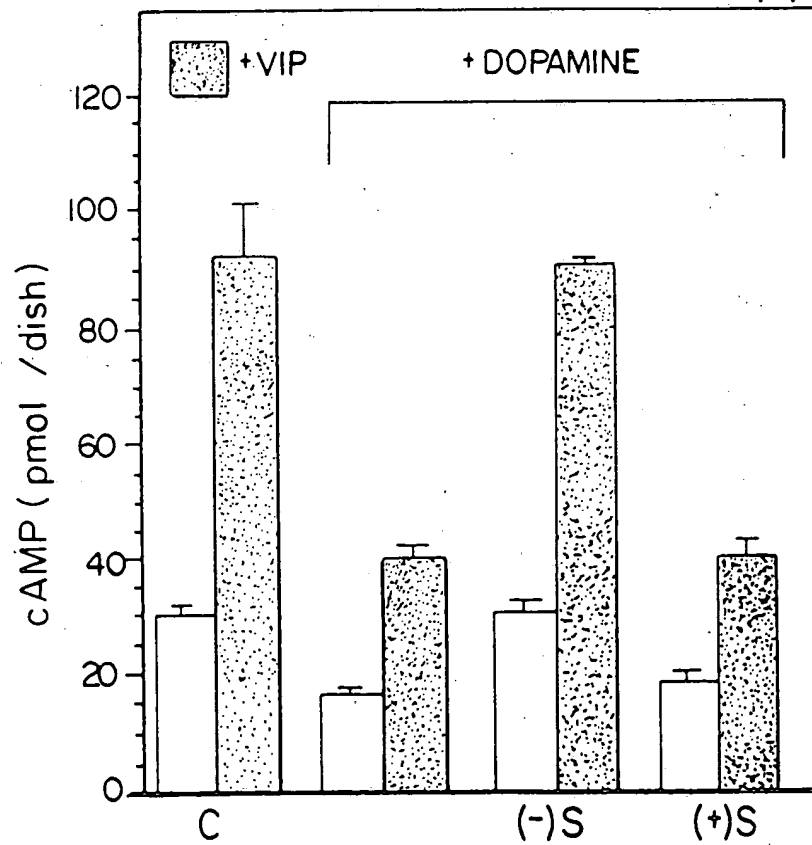
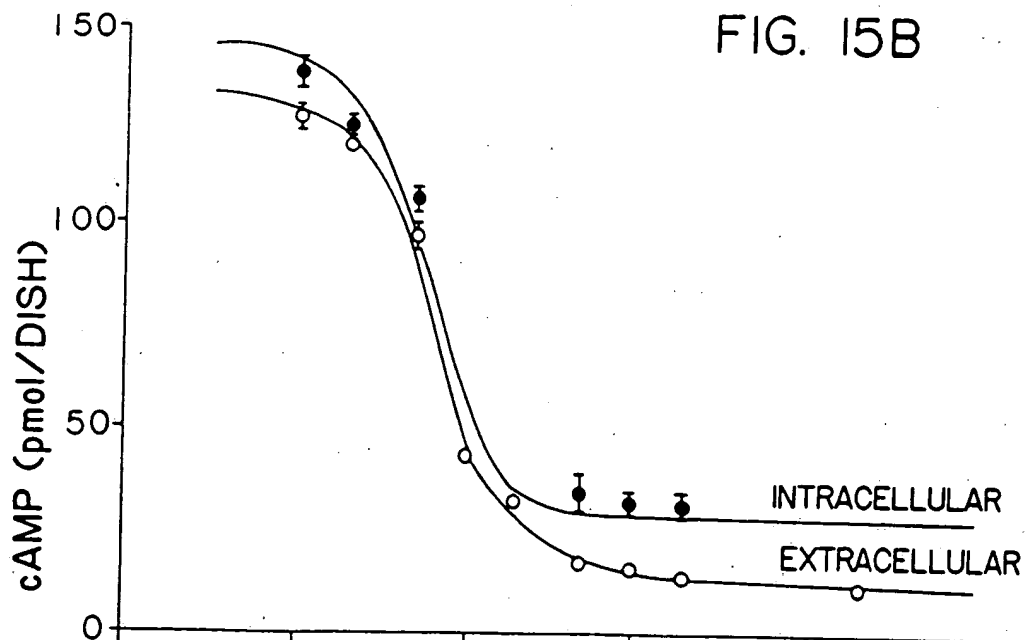
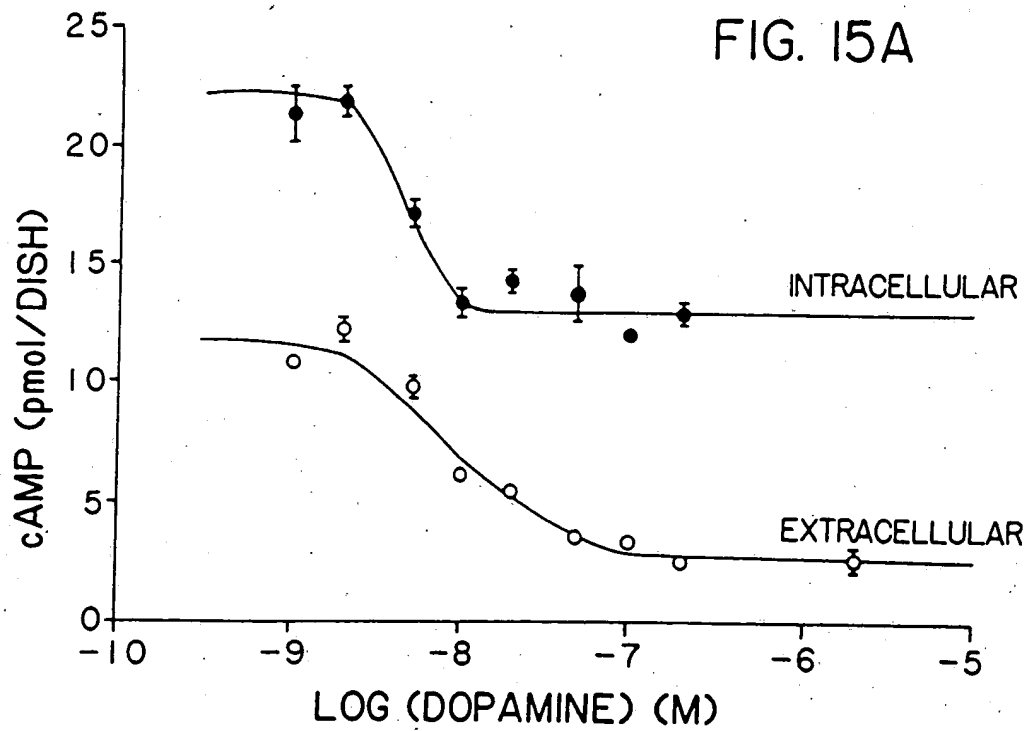


FIG.14B



2025 RELEASE UNDER E.O. 14176



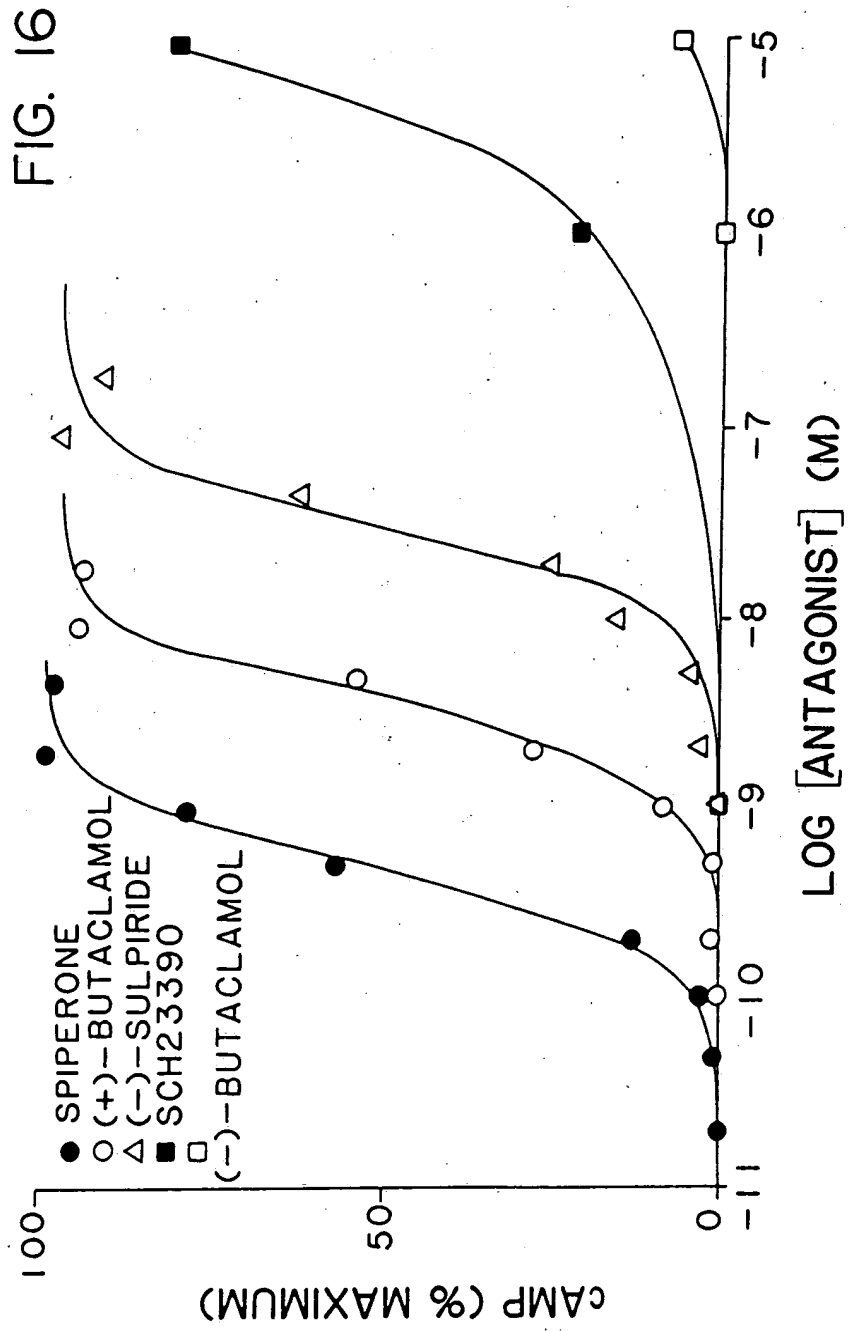


FIG.17A

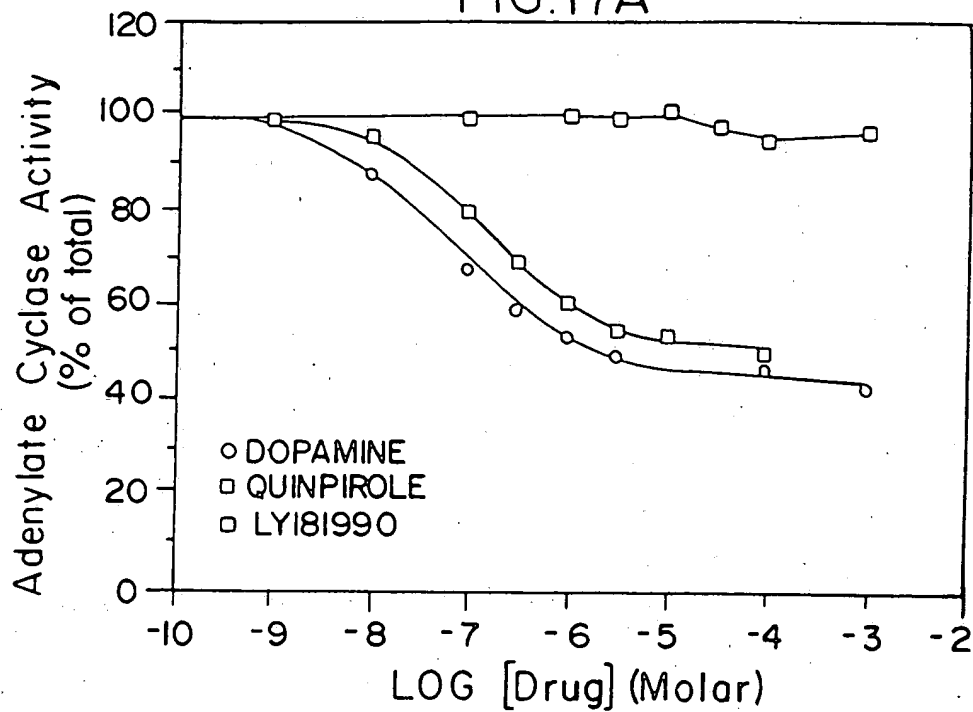
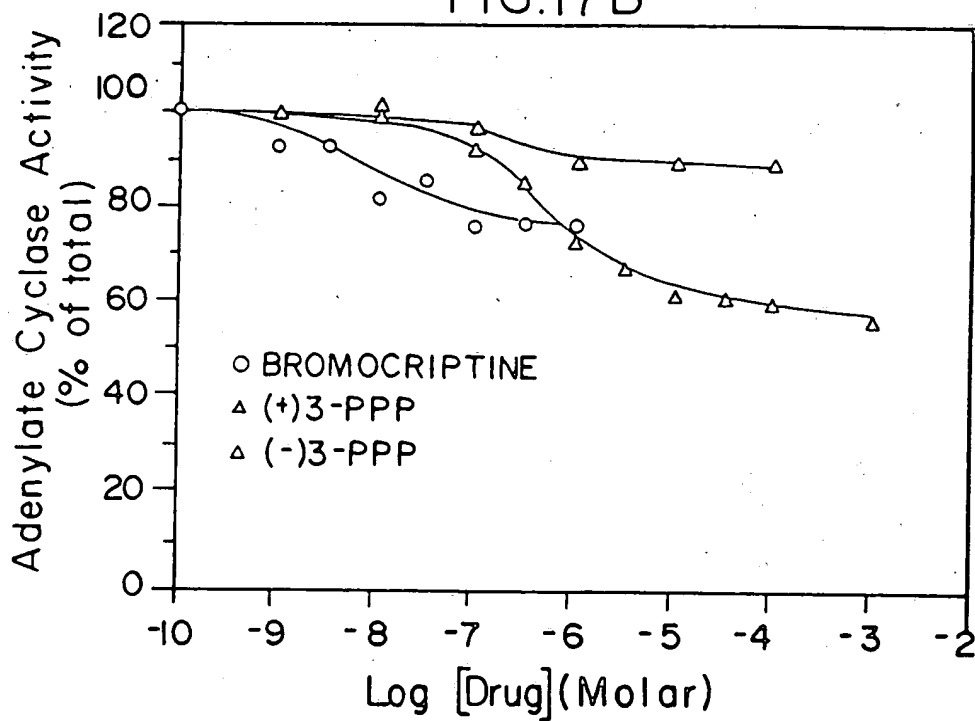


FIG.17B



[illegible]

FIG. 18B

110 120
 LysPheSerArgIleHisCysAspIlePheValThrLeuAspValMETMETCysThrAla
 AAATTCAGCAGGATTCACTGTGACATCTTCGTCACCTCTGGACGTCATGATGTGCCACGGCG
 360
 AAATTCAGCAGGATTCACTGTGACATCTTTGTCACTCTGGATGTCATGATGTGCCACAGCA

130 140
 SerIleLeuAsnLeuCysAlaIleSerIleAspArgTyrThrAlaValAlaMETProMET
 AGCATCCTGAACCTGTGTGCCATCAGCATCGACAGGTACACAGCTGTGGCCATGCCCATG
 AGCATCCTGAACCTGTGTGCCATCAGCATTGACAGGTACACAGCTGTGGCAATGCCCATG

150 160
 LeuTyrAsnThrArgTyrSerSerLysArgArgValThrValMETIleSerIleValTrp
 CTGTACAATACGGCTACAGCTCCAAGCGCCGGGTACCGTCATGATCTCCATCGTCTGG
 480
 CTGTATAACACACGCTACAGCTCCAAGCGCCGAGTTACTGTCAATGATGTCATGTCCTGG
 Ala

FIG. 18C

IV 170 180
ValLeuSerPheThrIleSerCysProLeuLeuPheGlyLeuAsnAsnAlaAspGlnAsn
 GTCCTGTCCTTCACCATCTCCTGCCACTCCTCTTCGGACTCAATAACGCAGACCAGAAC
 !!!
 GTCCTGTCCTTCACCATCTCCTGCCACTGCTCTTCGGACTCAACAATACAGACCAGAAAT
 Thr

190 V 200
 GluCysIleIleAlaAsnProAlaPheValValTyrSerSerIleValSerPheTyrVal
 GAGTGCATCATTTGCCAACCGCCTTCGTGGTCTACTCCTCCATCGTCTCCTTCTACGTG
 !!!!! !!!!!!!!!!!!! !!!!! !!!!!!!!!!!!! !!!!! !!!!!!!!!!!!!
 GAGTGTATCATTTGCCAACCCCTTGTGGTCTACTCCTCCATTGTCTCATTCTACGTG
 600

210 220
ProPheIleValThrLeuLeuValTyrIleLysIleTyrIleValLeuArgArgArg
 CCCTTCATTGTCAACCCTGCTGGTCTACATCAAGATCTACATTGTCTCCGCAGACGCCGC
 !!!!! !!!!! !!!!!!!!!!!!! !!!!! !!!!!!!!!!!!! !!!!! !!!!!
 CCCTTCATCGTCACTCTGCTGCTATATCAAAATCTACATCGTCTCCGGAAGCCCGG
 Lys

FIG. 18D

	290		300
METGluMETLeuSerSerThrSerProProGluArgThrArgTyrSerProIleProPro			
ATGGAGATGCTCTCCAGCACCCAGCCCGAGAGGACCCGGTACAGCCCATCCACCC			
IIIIIIIIII II IIIIIIIIIII II IIIIIIIIIII IIIIIIIIIII III			
ATGGAGATGCTCAAGCACCCAGCCCGCCAGAGAGGACCCGGTATAGCCCATCCCTCCC			
	310		320
SerHisHisGlnLeuThrLeuProAspProSerHisHisGlyLeuHisSerThrProAsp			
AGCCACCACGCTGACTCTCCCCGACCCGTCCTCCACCATGGTCTCCACAGCACTCCCGAC			
II IIIIIIIIIII IIIIIIIII II IIIIIIIII III IIIIIII III III			960
AGTCACCACGCTCACTCTCCCTGATCCATCCACCAACGGCCTACATAGCAACCTGAC			
		Asn	
	330		339
SerProAlaLysProGluLysAsnGlyHisAlaLys AspHisProLysIleAlaLys			
AGCCCCGCCAAACCCAGAGAAGAATGGGCATGCCAAA...GACCACCCCAAGATTGCCCAAG			
II II IIIIIIIIIII IIIIIIIIIII IIIII III IIIIIIIIIII			
AGTCCTGCCAAACCCAGAGAAGAATGGGCACGCCCAAGATTGTCAATCCAGGATTGCCCAAG			
		IleValAsn Arg	

FIG. 18F

IlePheGluIleGlnThrMETProAsnGlyLysThrArgThrSerLeuLysThrMETSer
ATCTTTGAGATCCAGACCATGCCCAATGGCAAACC CGACCTCCCTCAAGACCATGAGC
TT
TTCTTTGAGATCCAGACCATGCCCAATGGCAAACC CGACCTCCCTTAAGACCATGAGC
Phe

ArgArgLysLeuSerGlnGlnLysGluLysLysAlaThrGlnMETLeuAlaIleValLeu 369 379

[illegible]

FIG. 18G

409 VII 419
AspCysAsnIleProProValLeuTyrSerAlaPheThrTrpLeuGlyTyrValAsnSer

GACTGCAACATCCCGCCTGTCTGTACAGCGCCTTCACGTGGCTGGGCTATGTCAACAGC
 II IIIIIIIIIII II IIIII IIIIIIIIIII IIIIIIIIIIIIIIIIIIIIIII
 GATTGCAACATCCACCAAGTCCCTCTACAGCGCCTTCACATGGCTGGGCTATGTCAACAGT

429 439
AlaValAsnProIleIleTyrThrThrPheAsnIleGluPheArgLysAlaPheLeuLys

GCCGTGAACCCCATCATCTACACCACTTCAACATTGAGTTCCGCAAGGCCCTTCCTGAAG
 IIIII IIIIIIIIIIIIIIIIIIIIIIIII IIIIIIIIIIIIIIIIIIIIIII 1317
 GCCGTCAACCCCATCATCTACACCACTTCAACATCGAGTTCCGCAAGGCCCTTCATGAAG
 MET

IleLeuHisCys *
 ATCCTCCACTGCTGACTCTGCTGCCCTGCCCGCACAGCAGCCTGCTTCCACCTCCCTGCC
 IIII I IIIIIIIIIII
 ATCTTGCACTGCTGA

FIG. 18H

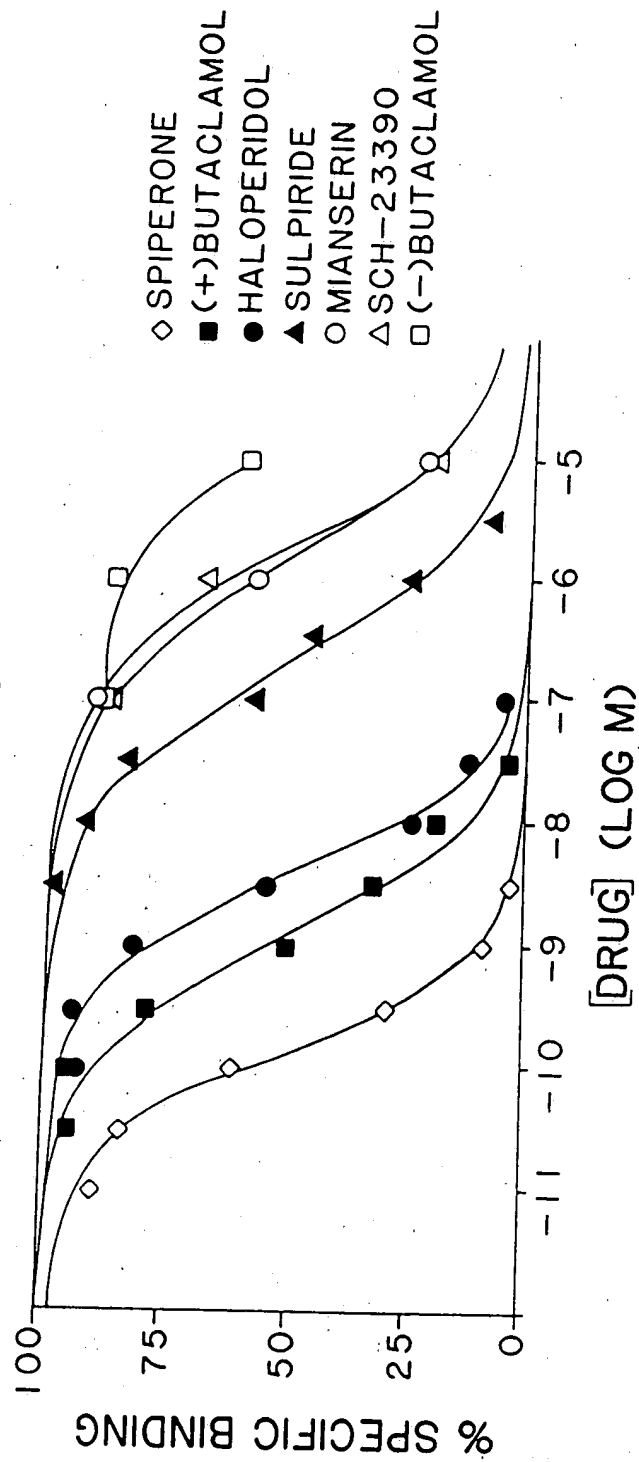
CAGGCCGGCCAGCCTCACCCCTTGCGAACCGTGAGCAGGAAGGCCCTGGGTGGATCGGCCTC 1437
 CTCCTTCTTAGCCCCGGCAGGCCCTGCAGTGTTCGCTTGGCTCCATGCTCCTCACTGCCCG
 CACACCCCTCACTCTGCCAGGGCAGTGCTAGTGAGCTGGGCATGTACCAAGCCCTGGGGCT 1557
 GGGCCAGCTCAGGGGCAGCTCATAGAGTCCCCCCTCCACCTCCAGTCCCCCTATCCTT
 GGCACCAAGATGCAGCGCCCTTCCTTGACCTTCCTCTGGGGCTCTAGGTTGCTGGAGC 1677
 CTGAGTCAGGGCCAGAGGCTGAGTTTCTCTTTGTGGGGCTTGGCGTGGAGCAGCGCGT
 GGGGAGAGATGGACAGTTCACACCCCTGCAAGGCCACAGGAGGCAAGCAAGCTCTCTTGC 1797
 CGAGGAGCCAGGCAACTCAGTCCTGGGAGACCCCATGTAAATACCAGACTGCAGGTTGGA
 CCCCAAGGATTCCCAAGCCAAAACCTTAGCTCCCTCCCGCACCCCGATGTGGACCTCTA 1917

FIG. 18I

CTTCCAGGCTAGTCCGGACCCACCTCACCCCGTTACAGCTCCCCAAGTGGTTTCCACAT
GCTCTGAGAAGAGAGCCCTCATCTTGAAGGGCCAGGAGGGTCTATGGGAGAGGAACT 2037
CCTTGGCCTAGCCACCCCTGCTGCCCTTCTGACGGCCCTGCAATGTATCCCTTCTCACAGC
ACATGCTGGCCAGCCTGGGGCCTGGCAGGAGGTGAGGCCCTGGAACTCTATCTGGGCCT 2157
GGGCTAGGACATCAGAGGTTCTTTGAGGAGTGCCTCTGCCACACTCTGACGCAAACC
ACTTCCCTTTCTATTCCCTTCTGGCCCTTCCCTCTCTCCTGTTTCCCTTCCCTCCACTGC 2277
CTCTGCCCTTAGAGGAGCCACGGCTAAGAGGCTGCTGAAAACCATCTGGCCTGGCCTGGC
CCTGCCCTGAGGAAGGAGGGCAAGCTGCAGCTTGGGAGAGCCCTGGGCCTAGACTCTG 2397
TAACATCACTATCCGATGCACCAAACTAATAAACTTTGACGAGTCACCTTC (A)_n 2449

FIG. 18J

FIG. 19



1 2 3 4

kb

—12.0

— 6.0

— 4.0

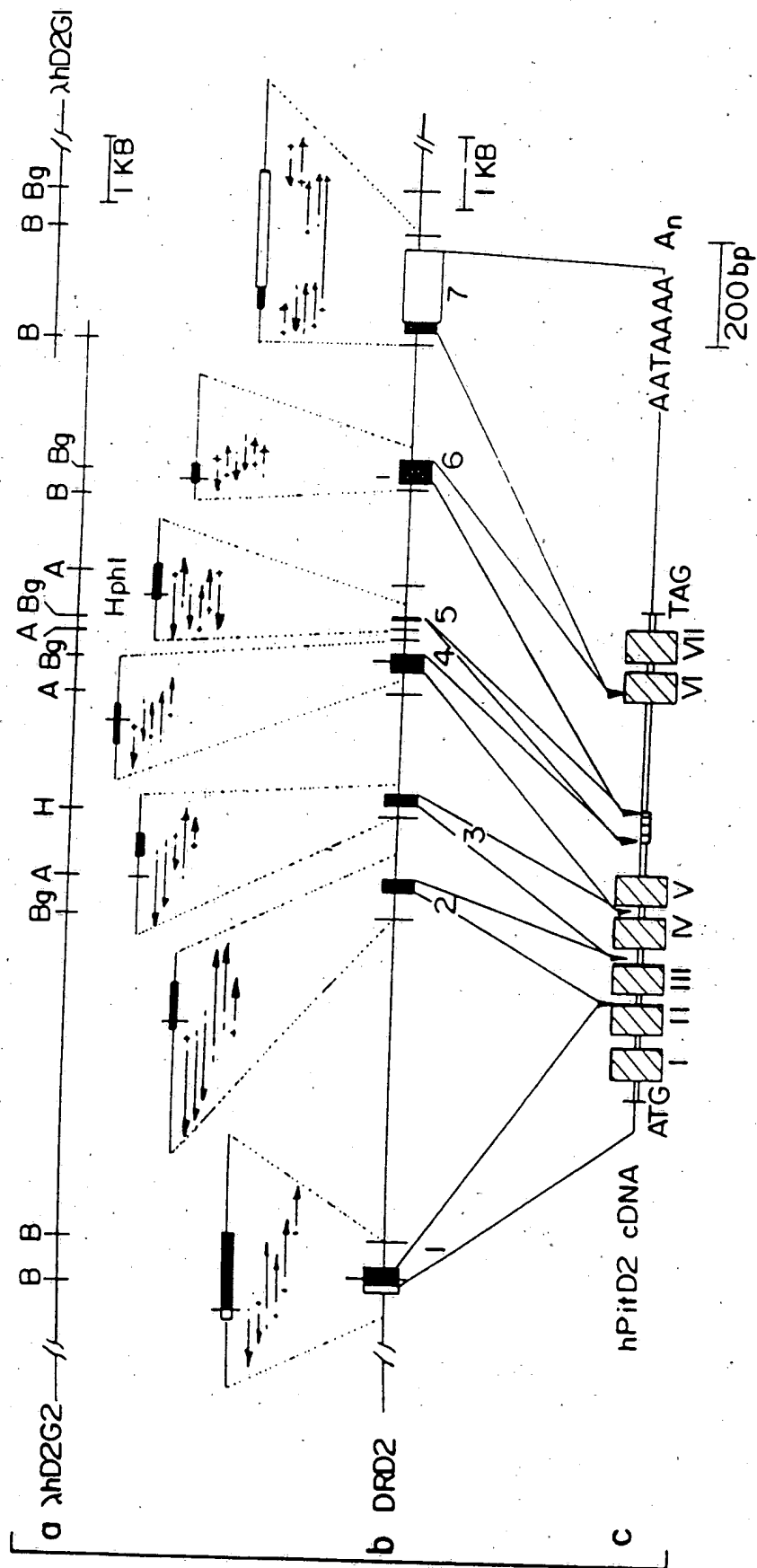
— 2.0

— 1.6

— 1.0

FIG. 20

FIG. 21



DRUG	HUMAN D ₂	RAT D ₂	RAT STRIATUM
PIPERONE	0.125	0.35	0.56
(+) BUTACLAMOL	0.94	1.2	1.6
HALOPERIDOL	2.4	5.1	5.8
SULPIRIDE	206	160	205
MIANSERIN (5-HT)	2685	4300	4600
SCH 23390 (D1)	2145	2500	3300
(+) BUTACLAMOL	>10,000	>10,000	>10,000
Kd [³ H] DOMPERIDONE	0.74	0.40	0.40

FIG. 22